FIG. 1

```
  -54   AGCTGCGGCCCGGTCTGCCAGCCAGACCCTTTGGAGAAGAACCCCACTCCCTGTC
  1 ATGGGCCCCCGCTGCACCCTGCACCCCCTTTCTCTCCTGGTGCAGGTGACAGCGCTGGCT 60
    M  G  P  R  C  T  L  H  P  L  S  L  L  V  Q  V  T  A  L  A
 61 GCGACTCTGGCCCAGGGCAGGCTGCCTGCCTTCTGCCCTGTGAGCTCCAGCCCCACGGC 120
    A  T  L  A  Q  G  R  L  P  A  F  L  P  C  E  L  Q  P  H  G
121 CTGGTGAACTGCAACTGGCTCTTCCTGAAGTCCGTGCCCCACTTCTCGGCGGCAGCGCCC 180
    L  V  N  C  N  W  L  F  L  K  S  V  P  H  F  S  A  A  A  P
181 CGGGCCAACGTCACCAGCCTCTCCTTACTCTCCAACCGGCATCCACCACTTGCACGACTCT 240
    R  A  N  V  T  S  L  S  L  L  S  N  R  I  H  H  L  H  D  S
241 GACTTCGTCCACCTGTCCAGCCTACGAACTCTCAACCTCAAGTGGAACTGCCCGCCGGCT 300
    D  F  V  H  L  S  S  L  R  T  L  N  L  K  W  N  C  P  P  A
301 GGCCTCAGCCCCATGCACTTCCCCTGCCACATGACCATCGAGCCCAACACCTTCCTGGCC 360
    G  L  S  P  M  H  F  P  C  H  M  T  I  E  P  N  T  F  L  A
361 GTGCCCACCCTGGAGGAGCTGAACCTGAGCTACAACAGCATCACGACCGTGCCTGCCCTG 420
    V  P  T  L  E  E  L  N  L  S  Y  N  S  I  T  T  V  P  A  L
421 CCCGACTCCCTCGTGTCCCTGTCGCTGAGCCGCACCAACATCCTGGTGCTAGACCCCACC 480
    P  D  S  L  V  S  L  S  L  S  R  T  N  I  L  V  L  D  P  T
481 CACCTCACTGGCCTACATGCCCTGCGCTACCTGTACATGGATGGCAACTGCTACTACAAG 540
    H  L  T  G  L  H  A  L  R  Y  L  Y  M  D  G  N  C  Y  Y  K
541 AACCCCTGCCAGGGGCGCTGGAGGTGGTGCCGGGTGCCCTCCTCGGCCTGGCAACCTC 600
    N  P  C  Q  G  A  L  E  V  V  P  G  A  L  L  G  L  G  N  L
601 ACACATCTCTCACTCAAGTACAACAATCTCACGGAGGTGCCCCGCAGCCTGCCCCCCAGC 660
    T  H  L  S  L  K  Y  N  N  L  T  E  V  P  R  S  L  P  P  S
661 CTCGAGACCCTGCTGTTGTCCTACAACCACATTGTCACCCTGACGCCTGAGGACCTGGCC 720
    L  E  T  L  L  L  S  Y  N  H  I  V  T  L  T  P  E  D  L  A
721 AATCTGACTGCCCTGCGCCGTGCTTGATGTGGGGGGGGAACTGCCGCCCCTGTGACCATGCC 780
    N  L  T  A  L  R  V  L  D  V  G  G  N  C  R  R  C  D  H  A
```
(SEQ ID NO:1 1-834)
(SEQ ID NO:2 1-260)

FIG. 2

```
 781  CGCAACCCCTGCAGGGAGTGCCCAAAGGACCACCCCAAGCTGCACTCTGACACCTTCAGC  840
       R   N   P   C   R   E   C   P   K   D   H   P   K   L   H   S   D   T   F   S

 841  CACCTGAGCCGGCCTCGAAGGCCTGGTGTTGAAAGACAGTTCTCTCTACAACCTGGACGCC  900
       H   L   S   R   L   E   G   L   V   L   K   D   S   S   L   Y   N   L   D   A

 901  AGGTGGTTCCGAGGCCTGGACAGGCTCCAAGTGCTGGACCTGAGTGAGAACTTCCTCTAC  960
       R   W   F   R   G   L   D   R   L   Q   V   L   D   L   S   E   N   F   L   Y

 961  GACTGCATCACCAAGACCACGGCCTTCCAGGGCCTGGCCCGACTgCGCcAAGCTCAACCTG 1020
       D   C   I   T   K   T   T   A   F   Q   G   L   A   R   L   R   K   L   N   L

1021  TCCTTCAATTACCACAAGAAGGTGTCCTTTGCCCACTGCACCTGGCACCCTCCTTTGGG  1080
       S   F   N   Y   H   K   K   V   S   F   A   H   L   H   L   A   P   S   F   G

1081  CACCTCCGGTCCCTGAAGGAGCTGGACATGCATGGCATCTTCTTCCGCTCGCTCAGTGAG 1140
       H   L   R   S   L   K   E   L   D   M   H   G   I   F   F   R   S   L   S   E

1141  ACCACGCTCCAACCTCTGGTCCAACTGCCTATGCTCCAGACCCTGCGCCTGCAGATGAAC 1200
       T   T   L   Q   P   L   V   Q   L   P   M   L   Q   T   L   R   L   Q   M   N

1201  TTCATTAACCAGCCCAGCCTCAGCATCTTTGGGGCCTTCCCTGGCCTGCTGTACGTGGAC 1260
       F   I   N   Q   A   Q   L   S   I   F   G   A   F   P   G   L   L   Y   V   D

1261  CTATCGGACAACCGCATCAGCGGGAGCTGCAAGGCCAGTGGCCATTACTAGGGAGGTGGAT 1320
       L   S   D   N   R   I   S   G   A   A   R   P   V   A   I   T   R   E   V   D

1321  GGTAGGGAGAGGGTCTGGCTGCCTTCCAGGAACCTCGCTCCACGTCCACTGGACACTCTC 1380
       G   R   E   R   V   W   L   P   S   R   N   L   A   P   R   P   L   D   T   L

1381  CGCTCAGAGGACTTCATGCCAAACTGCAAGGCCTTCAGCTTCACCTTGGACCTGTCTCGG 1440
       R   S   E   D   F   M   P   N   C   K   A   F   S   F   T   L   D   L   S   R

1441  AACAACCTGGTGACAATCCAGTCGGAGATGTTTGCTGCCCTCTCACGCCTCGAGTGCCTG 1500
       N   N   L   V   T   I   Q   S   E   M   F   A   R   L   S   R   L   E   C   L

1501  CGTCTGAGCCACAACAGCATCTCCCAGGCGGTCAATGGCTCTCAGTTTGTGCCGCTGACC 1560
                                                (SEQ ID NO:1  835-1614)
       R   L   S   H   N   S   I   S   Q   A   V   N   G   S   Q   F   V   P   L   T
                                                (SEQ ID NO:2  261-520)
```

FIG. 3

```
1561 AGCCTGCGGGTGCTGGACCTGTCCCACAACAAGCTGGACCTGTATCACGGGCGCTCGTTC 1620
      S   L   R   V   L   D   L   S   H   N   K   L   D   L   Y   H   G   R   S   F

1621 ACGGAGCTGCCCGCGCCTGGAAGCACTGGACCTCAGCTACAACAGCCAGCCCTTTACCATG 1680
      T   E   L   P   R   L   E   A   L   D   L   S   Y   N   S   Q   P   F   T   M

1681 CAGGGTGTGGGCCACAACCTCAGCTTCGTGGCCCAGCTGCCCGCCCTGCGCTACCTCAGC 1740
      Q   G   V   G   H   N   L   S   F   V   A   Q   L   P   A   L   R   Y   L   S

1741 CTGGCGCACAATGACATCCATAGCCGAGTGTCCCAGCAGCTCTGTAGCGCCTCACTGTGC 1800
      L   A   H   N   D   I   H   S   R   V   S   Q   Q   L   C   S   A   S   L   C

1801 GCCCTGGACTTTAGCGGCAACGATCTGAGCCGGATGTGGGCTGAGGGAGACCTCTATCTC 1860
      A   L   D   F   S   G   N   D   L   S   R   M   W   A   E   G   D   L   Y   L

1861 CGCTTCTTCCAAGGCCTAAGAAGCCTAGTCTGGCTGGACCTGTCCCAGAACCACCTGCAC 1920
      R   F   F   Q   G   L   R   S   L   V   W   L   D   L   S   Q   N   H   L   H

1921 ACCCTCCTGCCACGTGCCCTGGACAACCTCCCCAAAAGCCTGAAGCATCTGCATCTCCGT 1980
      T   L   L   P   R   A   L   D   N   L   P   K   S   L   K   H   L   H   L   R

1981 GACAATAACCTGGCCTTCTTCAACTGGAGCAGCCTGACCCTCCTGCCCAAGCTGGAAACC 2040
      D   N   N   L   A   F   F   N   W   S   S   L   T   L   L   P   K   L   E   T

2041 CTGGACTTGGCTGGAAACCAGCTGAAGGCCCTAAGCAATGGCAGCCTGCCATCTGGCACC 2100
      L   D   L   A   G   N   Q   L   K   A   L   S   N   G   S   L   P   S   G   T

2101 CAGCTGCGGGAGGCTGGACCTCAGTGGCAACAGCATCGGCTTTGTGAACCCTGGCTTCTTT 2160
      Q   L   R   R   L   D   L   S   G   N   S   I   G   F   V   N   P   G   F   F

2161 GCCCTGGCCAAGCAGTTAGAAGAGCCTCAACCTCAGCGGCCAATGCCCTCAAGACAGTGGAG 2220
      A   L   A   K   Q   L   E   E   L   N   L   S   A   N   A   L   K   T   V   E

2221 CCCTCCTGGTTTGGCTCGATGGTGGGCAACCTGAAAGTCCTAGACGTGAGCGCCAACCCT 2280
      P   S   W   F   G   S   M   V   G   N   L   K   V   L   D   V   S   A   N   P

2281 CTGCACTGCGCCTGTGGGGCGACCTTCGTGGGCTTCCTGCTGGAGGTACAGGCTGCCGTG 2340
      L   H   C   A   C   G   A   T   F   V   G   F   L   L   E   V   Q   A   A   V
```
(SEQ ID NO:1 1615-2394)
(SEQ ID NO:2 521-780)

FIG. 4

```
2341 CCTGGGCTGCCCAGCCGCGTCAAGTGTGGCAGTCCGGGGCAGCTCCAGGGCCATAGCATC 2400
        P   G   L   P   S   R   V   K   C   G   S   P   G   Q   L   Q   G   H   S   I
2401 TTTGCGCAAGACCTGCGCCTCTGCCTGGATGAGACCCTCTCGTGGAACTGTTTTGGCATC 2460
        F   A   Q   D   L   R   L   C   L   D   E   T   L   S   W   N   C   F   G   I
2461 TCGCTGCTGGCCATGGCCCTGGGCCTGGTTGTGCCCATGCTGCACCACCTCTGCGGCTGG 2520
        S   L   L   A   M   A   L   G   L   V   V   P   M   L   H   H   L   C   G   W
2521 GACCTCTGGTACTGCTTCCACCTGTGCCTGGCCTGGCTGCCCCACCGAGGGCAGGGCCGG 2580
        D   L   W   Y   C   F   H   L   C   L   A   W   L   P   H   R   G   Q   R   R
2581 GGCGCAGACGCCCTGTTCTATGATGCCTTCGTGGTCTTTGACAAAGCTCAGAGTGCTGTG 2640
        G   A   D   A   L   F   Y   D   A   F   V   V   F   D   K   A   Q   S   A   V
2641 GCCGACTGGGTGTACAACGAGCTGCGGGTGCAGCTGGAGGAGCGCCGTGGGCGCCGCGCA 2700
        A   D   W   V   Y   N   E   L   R   V   Q   L   E   E   R   R   G   R   R   A
2701 CTGCGCCTGTGCCTGGAGGAGCGAGACTGGTTACCTGGCAAGACGCTCTTCGAGAACCTG 2760
        L   R   L   C   L   E   E   R   D   W   L   P   G   K   T   L   F   E   N   L
2761 TGGGCCTCAGTCTACAGCAGCCGCAAGACCCTGTTTGTGCTGGCCCACACGGACCGTGTC 2820
        W   A   S   V   Y   S   S   R   K   T   L   F   V   L   A   H   T   D   R   V
2821 AGCGGCCTCTTGCGTGCCAGTTTCCTGCTGGCCCAGCAGCGCCTGCTGGAGGACCGCAAG 2880
        S   G   L   L   R   A   S   F   L   L   A   Q   Q   R   L   L   E   D   R   K
2881 GACGTTGTAGTGCTGGTGATCCTGCGCCCCGATGCCTACCGCTCCCGCTACGTGCGGCTG 2940
        D   V   V   V   L   V   I   L   R   P   D   A   Y   R   S   R   Y   V   R   L
2941 CGCCAgCGGCTCTGCCGCCAGAGTGTCCTCCTCTGGCCCCACCAGCCCGGTGGGCAGGGC 3000
        R   Q   R   L   C   R   Q   S   V   L   L   W   P   H   Q   P   R   G   Q   G
3001 AGCTTCTGGGCCCAGCTGGGCACAGCCCTGACCAGGGACAACCGCCACTTCTATAACCGG 3060
        S   F   W   A   Q   L   G   T   A   L   T   R   D   N   R   H   F   Y   N   R
3061 AACTTCTGCCGGGGCCCCACGACAGCCGAATAG   3093 (SEQ ID NO:1 2395-3147)
        N   F   C   R   G   P   T   T   A   E   *        (SEQ ID NO:2 781-1030)
```

FIG. 6

```
SWINE    1 MGPRCT--LHPLSLLVQVTALAATLAQGRLPAFLPCELQPHGLVNCNWLFLKSVPHFSAA   58 SWINE
HUMAN    1 MGP-CRSALHPLSLLVQAIMLAMTLALGTLPAFLPCELQPHGLVNCNWLFLKSVPHFSMA   59 HUMAN
MOUSE    1 MVLRRRT-LHPLSLLVQAAVLAETLALGTLPAFLPCELKPHGLVDCNWLFLKSVPRFSAA   59 MOUSE
CAT      1 MGP-CHGALHPLSLLVQAAALAVALAQGTLPAFLPCELQRHGLVNCDWLFLKSVPHFSAA   59 CAT
           *,  ,   ********.  **  ,** *,********* ,****,*,*******,**,*

SWINE   59 APRANVTCLSLLCNRIHHLHDSDFVHLSSLRCTNLKWNCPPAGLSPMHFPCHMIIEPNTF  118 SWINE
HUMAN   60 APRGNVTCLSLSSNRIHHLHDSDFAHLPSLRHINLKWNCPPVGLSPMHFPCHMIIEPSTF  119 HUMAN
MOUSE   60 ASCQNITRLSLIGNRIHHLHNSDFVHLSNLRQINLKWNCPPTGLSPLHFSCHMIIEPRTF  119 MOUSE
CAT     60 APRGNVTCLSLYSNRIHHLHDSDFVHLSSLRRINLKWNCPPASLSPMHFPCHMIIEPHTF  119 CAT
           *,, ,* *,*** ********,***,**,,** ********* ,***,**,*******,**

SWINE  119 IAVPTLEEINLSYNSITTVPALPDSLVSLSLSRINILVLDPTHLTGLHAIRYLYMDGNCY  178 SWINE
HUMAN  120 LAVPTLEEINLSYNNIMTVPALPKSLISLSLSHTNIMLDGASLAGLHAIRFLFMDGNCY  179 HUMAN
MOUSE  120 LAMRTLEEINLSYNGITTVPRLPSSLVNLSLSHTNILVLDANSIAGLYSIRVLFMDGNCY  179 MOUSE
CAT    120 LAVPTLEEINLSYNSITTVPALPSSLVSLSLSRTNILVLDPAMLAGLHSIRFLFLDGNCY  179 CAT
           **,,*********,*,***,** **,,**** ****,**   *,**, ** *,,*****

SWINE  179 YKNPCQGALEVVPGALLGLGNLTHLSLKYNNLTEVPRSLPPSLETLLLSYNHIVTLTPED  238 SWINE
HUMAN  180 YKNPCRQAIEVAPGALLGLGNLTHLSLKYNNLTVWPRNLPSSLEYLLLSYNRIVKLAPED  239 HUMAN
MOUSE  180 YKNPCTGAVKVTPGALLGLSNLTHLSLKYNNLTKVPRQLPPSLEYLLVSYNLIVKLGPED  239 MOUSE
CAT    180 YKNPCPQALQVAPGALLGLGNLTHLSLKYNNLTAVPRGLPPSLEYLLLSYNHIITLAPED  239 CAT
           ***** *, * *******,************ *** **,***,**,*** *, * ***

SWINE  239 IANLTALRVLDVGGNCRRCDHARNPCRECPKDHPKLHSDTFSHLSRLEGLVLKDSSLYNL  298 SWINE
                                                        (SEQ ID NO:2  1-298)
HUMAN  240 IANLTALRVLDVGGNCRRCDHAPNPCMECPRHFPQLHPDTFSHLSRLEGLVLKDSSLSWL  299 HUMAN
                                                        (SEQ ID NO:4  1-299)
MOUSE  240 IANLTSLRVLDVGGNCRRCDHAPNPCIEQGQKSLHLHPETFHHLSHLEGLVLKDSSLHTL  299 MOUSE
                                                        (SEQ ID NO:6  1-299)
CAT    240 IANLTALRVLDVGGNCRRCDHARNPCMECPKGFPHLHPDTFSHLNHLEGLVLKDSSLYNL  299 CAT
           *****,*************** *** **,  , **,,**,**, ***********,*
                                                        (SEQ ID NO:8  1-299)
```

FIG. 7

```
SWINE  299 DARWFRGLDRLQVLDLSENFLYDCITKTTAFQGLARLRKLNLSFNYHKKVSFAHLHIAPS 358
HUMAN  300 NASWFRGLGNLRVLDLSENFLYKCITKTKAFQGLTQLRKLNLSFNYQKRVSFAHLSIAPS 359
MOUSE  300 NSSWFQGLVNLSVLDLSENFLYESINHINAFQNLTRLRKLNLSFNYRKKVSFARLHLASS 359
CAT    300 NPRWFHALGNLMVLDLSENFLYDCITKTTAFQGLAQLRRLNLSFNYHKKVSFAHLHLAPS 359
               .  ** . *  . * ********* ._. * *** . * ** .******* * .**** .* ** .*

SWINE  359 FGHLRSLKELDMHGIFFRSLSETTLQPLVQLPMLQTLRLQMNFINQAQLSIFGAFPGLLY 418
HUMAN  360 FGSLVAIKELDMHGIFFRSLDETTLRPLARLPMLQTLRLQMNFINQAQLGIFRAFPGLRY 419
MOUSE  360 FKNLVSLQELNMNGIFFRSLNKYTLRWLADLPKLHTLHLQMNFINQAQLSIFGTFRALRF 419
CAT    360 FGSLLSLQQLDMHGIFFRSLSETTLRSLVHLPMLQSLHLQMNFINQAQLSIFGAFPGLRY 419
               *. . *  . * *  . * ******* ..** . *  ** .. * *********** .** ..* .* ..

SWINE  419 VDLSDNRISGAARPVAITREVDGR-ERVWLPSRNLAPRPLDTLRSEDFMPNCKAFSFTLD 477
HUMAN  420 VDLSDNRISGASELTATMGEADGG-EKVWLQPGDLAPAPVDTPSSEDFRPNCSTLNFTLD 478
MOUSE  420 VDLSDNRISGPSTLSEATPEEADDAEQEELLSADPHPAPLSTPASKNFMDRCKNFKFTMD 479
CAT    420 VDLSDNRISGAMELAAATGEVDGG-ERVRLPSGDLALGPPGTPSSEGFMPGCKTLNFTLD 478
               **********,  .  .  .  .*  .. * .* .* . ....*  *. * .* *.. *.  ** .*

SWINE  478 LSRNNLVTIQGEMFARLSRLECLRLSHNSISQAVNGSQFVPLTSLRVLDLSHNKLDLYHG 537
                                            (SEQ ID NO:2 299-537)
HUMAN  479 LSRNNLVTVQPEMFAQLSHLQCLRLSHNCISQAVNGSQFLPLTGLQVLDLSRNKLDLYHE 538
                                            (SEQ ID NO:4 300-538)
MOUSE  480 LSRNNLVTIKPEMFVNLSRLQCLSLSHNSIAQAVNGSQFLPLINLQVLDLSHNKLDLYHW 539
                                            (SEQ ID NO:6 300-539)
CAT    479 LSRNNLVTIQPEMFARLSRLQCLLLSRNSISQAVNGSQFMPLTSLQVLDLSHNKLDLYHG 538
               ******** ..  .    ***  . ** . * ** .* . *  ******** *** . *   ***** *******
                                            (SEQ ID NO:8 300-538)
```

FIG. 8

```
SWINE   538 RSFTELPRLEALDLSYNSQPFTMQGVGHNLSFVAQLPALRYLSLAHNDIHSRVSQQLCCA 597
HUMAN   539 HSFTELPRLEALDLSYNSQPFGMQGVGHNFSFVAHLRTLRHLSLAHNNIHSQVSQQLCST 598
MOUSE   540 KSFSELPQLQALDLGYNSQPFSIKGIGHNFSFVAHLGMLHSLSLAHNDIHTRVSSHLNSN 599
CAT     539 RSFTELPRLEALDLSYNSQPFSMQGVGHNLSFVAQLPALRYLSLAHNDIHSRVSQQLCCA 598
                ** *** * **** ******  ** *** ****  *   *  ****** ** * ** * *

SWINE   598 SLCALDFSGNDLSRMWAEGDLYLRFFQGLRSLVWLDLSQNHLHTLLPRALDNLPKSLKHL 657
HUMAN   599 SLRALDFSGNALGHMWAEGDLYLHFFQGLSGLIWLDLSQNRLHTLLPQTLRNLPKSLQVL 658
MOUSE   600 SVRFLDFSGNGVGFMWADEGGLYLHFFQGLSGLLKLDLSQNLHILFPQNLDNLPKSLKLL 659
CAT     599 SLRALDFSGNALSRMWAEGDLYLXFFRGLRSLVRLDLSQNRLHTLLPRTLDNLPKSLRLL 658
                *  *  ******  *  ** **  *** ** **  *  ****** ** * *  * ****** *

SWINE   658 HLRDNNLAFFNWSSLTLLPKLETLDLAGNQLKALSNGSLPSGTQLRRLDLSGNSIGFVNP 717
HUMAN   659 RLRDNYLAFFKWWSLHFLPKLEVLDLAGNRLKALTNGSLPAGTRLRRLDVSCNSISFVAP 718
MOUSE   660 SLRDNYLSFFNWTSLSFLPNLEVLDLAGNQLKALTNGTLPNGTLLQKLDVSSNSIVSVVP 719
CAT     659 RLRDNYLAFFNWSSLVLLPRLEALDLAGNQLKALSNGSLPNGTQLRRLDLSSNSISFVAS 718
                ****  * ** ** **  ** ** ****** ****  ** **  ** * *  ** * *** *

SWINE   718 GFFALAKQLEEINLSANALKTVEPSWFGGMVGNLKVLDVSANPLHCACGATFVGFLLEVQ 777
HUMAN   719 GFFSKAKELFEINLSANALKTVDHSWFGPLASALQILDVSANPLHCACGAAFMDFLLEVQ 778
MOUSE   720 AFFALAVEIKEVNLSHNILKTVDRSWFGPIVMNLTVLDVRSNPLHCACGAAFVDLLLEVQ 779
CAT     719 SFFALATRLFEINLSANALKTVEPSWFGSLAGITLKVLDVTGNPLHCACGAAFVDFLLEVQ 778
                **  * *  * *** * **** ****    *  *** ********** * *  ****

SWINE   778 AAVPCLPSRVKCGSPGQLQGHSIFAQDLRLCLDETLSWNCFGISLLAMALGLVVPMLHHL 837
                                              (SEQ ID NO:2 538-837)
HUMAN   779 AAVPGLPSRVKCGSPGQLQGLSIFAQDLRLCLDEALSWDCFALSLLIAVALGLGVPMLHHL 838
                                              (SEQ ID NO:4 539-838)
MOUSE   780 TKVPGLANGVKCGSPGQLQGRSIFAQDLRLCLDEVLSWDCFGLSLLIAVAVGMVVPILHHL 839
                                              (SEQ ID NO:6 540-839)
CAT     779 AAVPGLPGHVKCGSPGQLQGRSIFAQDLRLCLDEALSWDCFGLSLLITVALGLAVPMLHHL 838
                ..  ****  ********** ************ *** **  *** * *  ** ****
                                              (SEQ ID NO:8 539-838)
```

FIG. 9

```
SWINE   838 CGVDLWYCFHLCLAWLPHRGQRRGAD--ALFYDAFVVFDKAQSAVADWVYNELRVQLEER   895
HUMAN   839 CGWDLWYCFHLCLAWLPWRGRQSGRDEDALPYDAFVVFDKTQSAVADWVYNELRGQLEEC   898
MOUSE   840 CGWDVWYCFHLCLAWLPLLARSRRSAQA-LPYDAFVVFDKAQSAVADWVYNELRVRLEGR   898
CAT     839 CGWDLWYCFHLCLAWLPRRGRRRGAD--ALPYDAFVVFDKAQSAVADWVYNELRVRLEER   896
                **** ************   ***  **    * ********* *************  **  ..

SWINE   896 RGRRALRLCLEERDWLPGKTLFENLWASVYSSRKTLFVLAHTDRVSGLLRASFLLAQQRL   955
HUMAN   899 RGRWALRLCLEERDWLPGKTLFENLWASVYGSRKTLFVLAHTDRVSGLLRASFLLAQQRL   958
MOUSE   899 RGRRALRLCLEDRDWLPGQTLFENLWASIYGSRKTLFVLAHTDRVSGLLRTSFLLAQQRL   958
CAT     897 RGRRALRLCLEERDWLPGKTLFENLWASVYSSRKMLFVLAHTDRVSGLLRASFLLAQQRL   956
                *** ******* ****** ********* * *** *************** ********

SWINE   956 LEDRKDVVVLVILRPDAYRSRYVRLRQRLCRQSVLLWPHQPRGQGSFWAQLGTALTRDNR 1015
HUMAN   959 LEDRKDVVVLVILSPDGRRSRYVRLRQRLCRQSVLLWPHQPSGQRSFWAQLGVALTRDNH 1018
MOUSE   959 LEDRKDVVVLVILRPDAHRSRYVRLRQRLCRQSVLFWPQQPNGQGGFWAQLSTALTRDNR 1018
CAT     957 LEDRKDVVVLVILRPDAHRSRYVRLRQRLCRQSVLLWPHQPSGQRSFWAQLGTALTRDNQ 1016
                ************ **  **************** **  ** **  *****  ******

SWINE  1016 HFYNRNFCRGPTTAE (SEQ ID NO:2 838-1030)                       1030
HUMAN  1019 HFYNRNFCQGP-TAE (SEQ ID NO:4 839-1032)                       1032
MOUSE  1019 HFYNQNFCRGP-TAE (SEQ ID NO:6 840-1032)                       1032
CAT    1017 HFYNQNFCRGPTTAE (SEQ ID NO:8 839-1031)                       1031
                **** *** ** ***
```